

## SEQUENCE LISTING

<110> Gray, Kevin A.  
Aboushadi, Nahla M.  
Garrett, James B.

<120> Amylases, Nucleic Acids Encoding them and Methods For Making and Using them

<130> 09010-091WO1

<140> not assigned

<141> 2003-10-15

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<151> 2002-10-31

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 Lys Lys Val Ala Ser Leu Asp Glu Asp Trp Glu Thr Thr Val Leu Tyr  
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 Gly Leu Ser Leu Leu Ser Tyr Asn Phe Leu Asp Ser Asp Asp Pro Ile  
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 Tyr Ala Thr Ile Asn Asp Lys Asn Lys Ala Asn Glu Tyr Ile Lys Trp  
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 Pro Glu Thr Phe Glu Pro Thr Ser Val Thr Pro Leu Val Trp Ser His  
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&lt;400&gt; 3

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&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Archaea

&lt;400&gt; 4

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&lt;211&gt; 1854

&lt;212&gt; DNA

&lt;213&gt; Archaea

&lt;400&gt; 5

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 35 40 45  
 Val Lys Trp His Trp Asp Asp Asp Trp Asp Ile Ser Gln Lys Tyr Ile  
 50 55 60  
 Glu Glu Thr Asn Ile Phe Lys Thr Ile Leu Glu Asp Asp Lys Ile Ile  
 65 70 75 80  
 Leu Thr Ile Lys Asp Phe Val Pro Val Ser His Asn Val Ile Ile Arg  
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 195 200 205  
 Ile Tyr Ile Leu Leu Gln Lys Phe Asp Gly Asp Leu Ser Ile Ile Thr  
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 225 230 235 240  
 Ser Met Asn Tyr Trp Lys Asn Ser Ile Gly Asn Ile Lys Glu His Ile  
 245 250 255  
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 260 265 270  
 Ala Leu Met Val Leu Leu Met Leu Cys Asp Lys Asp Gly Gly Ile Ile  
 275 280 285  
 Ala Ala Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Gly Arg Asp  
 290 295 300  
 Gly Ala Tyr Ile Ala Ile Ala Leu Asp Leu Phe Gly Ile Arg Gly Ile  
 305 310 315 320  
 Pro Asp Arg Phe Phe Glu Phe Met Ser Lys Ile Gln Asn Asp Asp Gly  
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 Ser Trp Leu Gln Asn Tyr Tyr Thr Asn Gly Lys Pro Arg Leu Thr Ala

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 Tyr Arg Leu Thr Gly Asn Arg Lys Phe Val Glu Arg Tyr Trp Asn Thr  
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 Ile Glu Lys Ala Gly Asn Tyr Leu Thr Ser Ala Ala Leu Asn Phe Thr  
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&lt;211&gt; 1866

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&lt;400&gt; 7

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 ctcaacaaga atttctggaa aagtagagta gatagcatgg taaataagtg gggaatctta 780  
 aagttggaag aatataaaga atgcatagat atatgcaaaa gatctctact aaccctatta 840  
 ctctctgcg attataaggg gggaataatt gcttctcctt ctttacatcc agattatagg 900  
 tatgtctggt gtagggatgc aggttatatg gcagttgcgt tggatttggt tgggcagcat 960  
 gaaatgagtg agaaatactt tgagtgggtc aagacaacac aaaacagtga cgggtcttgg 1020  
 gttcaaaatt actatgtgga ggggtatcca agattcacag ccatccaaat agatcagggtg 1080  
 ggtactacca ttggggcact tcttgtgcac tatagaataa ctggagacaa acattttta 1140  
 aaaagaaatt gggaaatggt caaaaaagca ggggactatt tgagcagagc tgctgaccaa 1200  
 ttaataccct gctatgactt atgggaagaa aagtttgggg tctttgcata taccctcgga 1260  
 gcaatatatg ggggggtgaa atcaggttat ttaattggaa aagaacttga caaagaagaa 1320  
 gaaatacagc attggaaaaa aagcatgaac ttccttaaaa atgaagtgtt aaatagactc 1380  
 tacttaaaaa atgagaagag gtttgcaaaa tcattaaaac cattagataa aaccatagat 1440  
 acgagtattt tagggtaag ttcccctat ggacttgtgt cagtcgatga cccaagaata 1500  
 atatcaactg caaatcagat tgaaaaagcc tcaactaca aagttgggtg tgttggtaga 1560  
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 aatggtatgt ttccagaaca agtcataaa gatttgggaa ttccaatata tgcaattccc 1800  
 cttggctggt cacatgcat ggttataatc gctattcatg gtgattacga catcctaata 1860  
 ccctaa 1866

&lt;210&gt; 8

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Archaea

&lt;400&gt; 8

Met Ala Gly Ile Ile Gly Asn Gly Asn Leu Leu Ala Lys Ile Asp Asp  
 1 5 10 15  
 Leu Gly Ser Ile Glu Tyr Ile Phe Phe Pro His Leu Gly Tyr Glu Thr  
 20 25 30  
 His Ile Leu Asp Thr Ser Phe Ala Ile Tyr Tyr Asn Asn Lys Ile Lys  
 35 40 45  
 Trp His Trp Asp His Ser Trp Asp Val Ser Gln Asn Tyr Leu Lys Asp  
 50 55 60  
 Ser Asn Ile Leu Lys Thr Thr Tyr Glu Asn Asp Asp Phe Leu Ile Tyr  
 65 70 75 80  
 Ser Lys Asp Cys Val Ser Ile Ser His Asn Leu Ile Val Lys Gln Leu  
 85 90 95  
 Ser Ile Ile Asn Lys Thr Asn Ser Glu Lys Asp Ile Lys Leu Phe Phe  
 100 105 110  
 Tyr Glu Asn Leu Arg Ile Gly Glu Thr Pro Ser Lys Ser Thr Val Lys  
 115 120 125  
 Phe Val Lys Glu Lys Asn Cys Leu Ile Lys His Asp Lys Asn Tyr Ile  
 130 135 140  
 Phe Cys Ile Gly Ser Asn Lys Lys Val Ser Ser Tyr Gln Cys Gly Ile  
 145 150 155 160  
 Lys Tyr Ser Glu Ser Ser Ala Leu Arg Asp Ile Glu Asn Gly Val Leu

165                      170                      175  
 Lys Glu Gln Ser Ser Ala Thr Gly Leu Ile Thr Asp Ser Ala Leu Cys  
 180                      185                      190  
 Trp Glu Phe Lys Ile Lys Pro Asn Gln Lys Tyr Thr Leu Ser Ile Leu  
 195                      200                      205  
 Ile Leu Pro Glu Lys Tyr Asp Gly Asp Tyr Asn Lys Thr Leu Asn Leu  
 210                      215                      220  
 Met Asp Thr Leu His Met Val Lys Asp Asn Leu Lys Asp Leu Tyr Asn  
 225                      230                      235                      240  
 Leu Thr Arg Asn Phe Trp Lys Ser Arg Val Asp Ser Met Val Asn Lys  
 245                      250                      255  
 Trp Gly Ile Leu Lys Leu Glu Glu Tyr Lys Glu Cys Ile Asp Ile Cys  
 260                      265                      270  
 Lys Arg Ser Leu Leu Thr Leu Leu Leu Leu Cys Asp Tyr Lys Gly Gly  
 275                      280                      285  
 Ile Ile Ala Ser Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Cys  
 290                      295                      300  
 Arg Asp Ala Gly Tyr Met Ala Val Ala Leu Asp Leu Cys Gly Gln His  
 305                      310                      315                      320  
 Glu Met Ser Glu Lys Tyr Phe Glu Trp Cys Lys Thr Thr Gln Asn Ser  
 325                      330                      335  
 Asp Gly Ser Trp Val Gln Asn Tyr Tyr Val Glu Gly Tyr Pro Arg Phe  
 340                      345                      350  
 Thr Ala Ile Gln Ile Asp Gln Val Gly Thr Thr Ile Trp Ala Leu Leu  
 355                      360                      365  
 Val His Tyr Arg Ile Thr Gly Asp Lys His Phe Leu Lys Arg Asn Trp  
 370                      375                      380  
 Glu Met Val Lys Lys Ala Gly Asp Tyr Leu Ser Arg Ala Ala Asp Gln  
 385                      390                      395                      400  
 Leu Ile Pro Cys Tyr Asp Leu Trp Glu Glu Lys Phe Gly Val Phe Ala  
 405                      410                      415  
 Tyr Thr Leu Gly Ala Ile Tyr Gly Gly Leu Lys Ser Gly Tyr Leu Ile  
 420                      425                      430  
 Gly Lys Glu Leu Asp Lys Glu Glu Glu Ile Gln His Trp Lys Lys Ser  
 435                      440                      445  
 Met Asn Phe Leu Lys Asn Glu Val Val Asn Arg Leu Tyr Leu Lys Asn  
 450                      455                      460  
 Glu Lys Arg Phe Ala Lys Ser Leu Lys Pro Leu Asp Lys Thr Ile Asp  
 465                      470                      475                      480  
 Thr Ser Ile Leu Gly Leu Ser Phe Pro Tyr Gly Leu Val Ser Val Asp  
 485                      490                      495  
 Asp Pro Arg Ile Ile Ser Thr Ala Asn Gln Ile Glu Lys Ala Phe Asn  
 500                      505                      510  
 Tyr Lys Val Gly Gly Val Gly Arg Tyr Pro Glu Asp Ile Tyr Phe Gly  
 515                      520                      525  
 Gly Asn Pro Trp Ile Ile Thr Thr Leu Trp Leu Tyr Met Tyr Tyr Lys  
 530                      535                      540  
 Lys Leu Val Asp Thr Leu Ser Lys Lys Gly Lys Phe Gln Glu Ser Ile  
 545                      550                      555                      560  
 Ile Asp Asn Tyr Asn Lys Lys Cys Tyr Asn Leu Leu Lys Trp Ile Leu  
 565                      570                      575

Lys His Gln Phe Asn Gly Met Phe Pro Glu Gln Val His Lys Asp Leu  
 580 585 590  
 Gly Ile Pro Ile Ser Ala Ile Pro Leu Gly Trp Ser His Ala Met Val  
 595 600 605  
 Ile Ile Ala Ile His Gly Asp Tyr Asp Ile Leu Ile Pro  
 610 615 620

<210> 9

> 1848

DNA

> Archaea

<210> 9

tttata tgggtggaat cgttggaac aatagttat tagccaaat tggagattat 60  
 aaattg aataccttt ttatcccaa gtgtgtatg aaactcatt cttgactct 120  
 ggcag ttatgataa aaaagtaaag tggcatiggg atgatgatt ggatataacc 180  
 aaatata ttgaggaaac gaacatattt aaaactatct tagaagatga taagattata 240  
 aaccatta aagattttgt gccagtatct cacaacgtgc ttataagaag agtgtatata 300  
 aaaaataaac tgataaaaa attaaatttt aagctctttt ttacgaaaa ttgagaatt 360  
 ggtgaaaacc caataacaaa tacagttaaa ttctagaag atggtgtat cgtaaatat 420  
 aatggaaaat atatttttg cattggaagt gataaaagaa tagattcatt tcagtgtgga 480  
 aatagataca gtaaaacaag tgcctacata gacatagaaa atgggatatt gaaggagcat 540  
 aaagagagtt ctggattatt aaccgatagt gcaatatcat ggaatataaa gattgatgaa 600  
 anaagaagtt tggcattcaa catctacata ctccacaaa gattcgatgg agattttca 660  
 ataataactg aacaactaaa gattataatg aataacagtg aaaacattaa aaatctctca 720  
 atgaattatt ggaaacatat tataggggag ataatagat ttatacatcc tgagcttagg 780  
 caaaataata agatttttc tataactaaa agggctttta tgacactttt aatgttatgt 840  
 gataaggaag gagggattat agcggtccca tctctacatc cagattatag atacgtgtgg 900  
 ggaagagatg gaagtatat ctcaattgct ttgacttat ttggcataag gaacattcca 960  
 gacagatttt ttgaattcat gtctaagata caaatgcag acggttcag gctacaaaat 1020  
 tattatgta atggaaaacc acgattaact gcaatacaga ctgaccaa attggtccata 1080  
 ttatgggcaa tggatgtgca ttacagatta actggggata gaaagttcgt tgagagatac 1140  
 tggaaacta tagagaaagc tgctaattat ttaagggttg tagctttaa cttactcca 1200  
 tgcttcgatt tgtgggaaga gaggtttgga gtatttgctt atacaatggg agctacttac 1260  
 gctggattga aatgtgcata cagcatgagt aaggcagtga ataaaaggga taaagttaag 1320  
 gattggggaa aaaccataga attttaaa catgagggtc caaagagatt ttatttgaa 1380  
 gatgaggaaa gatttgctaa atcaataaat ccttagaca agacgataga cacaagcata 1440  
 ttgggtttaa gttacccttt caatttgatt gatgtgatg atgagagaat gataaaaaca 1500  
 gccgaagcaa ttgaaaaagc ttcaaatat aaggttgagg ggattgggag atatccagaa 1560  
 gacatttact ttggaggcaa tccatggatt ataaccacat tatggcttcc ttgtattat 1620  
 agaaggttat acaaggtttt aaaagaaaaa gatgataatg ggcagatat ttatctaaa 1680  
 aaatctaaga agttgtttta ttgggtgatg aaatacagct ttgatgggct gttccagag 1740  
 caaatcata aagaattagg tgtccaatg tccgctatgc ctttaggctg gagcaatgca 1800  
 atgttctca ttatgtgta tgagaatgat aaggtcataa taccataa 1848

<210> 10

<211> 615

<212> PRT

<213> Archaea

<400> 10

Met Ile Tyr Met Gly Gly Ile Val Gly Asn Asn Ser Leu Leu Ala Lys  
 1 5 10 15  
 Ile Gly Asp Tyr Gly Glu Ile Glu Tyr Leu Phe Tyr Pro Gln Val Gly  
 20 25 30  
 Tyr Glu Thr His Phe Phe Asp Ser Ala Leu Ala Val Tyr Asp Lys Lys  
 35 40 45  
 Val Lys Trp His Trp Asp Asp Asp Trp Asp Ile Thr Gln Lys Tyr Ile  
 50 55 60  
 Glu Glu Thr Asn Ile Phe Lys Thr Ile Leu Glu Asp Asp Lys Ile Ile  
 65 70 75 80  
 Leu Thr Ile Lys Asp Phe Val Pro Val Ser His Asn Val Leu Ile Arg  
 85 90 95  
 Arg Val Tyr Ile Lys Asn Lys Leu Asp Lys Lys Leu Asn Phe Lys Leu  
 100 105 110  
 Phe Phe Tyr Glu Asn Leu Arg Ile Gly Glu Asn Pro Ile Thr Asn Thr  
 115 120 125  
 Val Lys Phe Leu Glu Asp Gly Cys Ile Val Lys Tyr Asn Gly Lys Tyr  
 130 135 140  
 Ile Phe Cys Ile Gly Ser Asp Lys Arg Ile Asp Ser Phe Gln Cys Gly  
 145 150 155 160  
 Asn Arg Tyr Ser Lys Thr Ser Ala Tyr Ile Asp Ile Glu Asn Gly Ile  
 165 170 175  
 Leu Lys Glu His Lys Glu Ser Ser Gly Leu Leu Thr Asp Ser Ala Ile  
 180 185 190  
 Ser Trp Asn Ile Lys Ile Asp Glu Lys Arg Ser Leu Ala Phe Asn Ile  
 195 200 205  
 Tyr Ile Leu Pro Gln Arg Phe Asp Gly Asp Phe Ser Ile Ile Thr Glu  
 210 215 220  
 Gln Leu Lys Ile Ile Met Asn Asn Ser Glu Asn Ile Lys Asn Leu Ser  
 225 230 235 240  
 Met Asn Tyr Trp Lys His Ile Ile Gly Glu Ile Asn Arg Phe Ile His  
 245 250 255  
 Pro Glu Leu Arg Gln Asn Asn Lys Ile Tyr Ser Ile Thr Lys Arg Ala  
 260 265 270  
 Leu Met Thr Leu Leu Met Leu Cys Asp Lys Glu Gly Gly Ile Ile Ala  
 275 280 285  
 Ala Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Gly Arg Asp Gly  
 290 295 300  
 Ser Tyr Ile Ser Ile Ala Leu Asp Leu Phe Gly Ile Arg Asn Ile Pro  
 305 310 315 320  
 Asp Arg Phe Phe Glu Phe Met Ser Lys Ile Gln Asn Ala Asp Gly Ser  
 325 330 335  
 Trp Leu Gln Asn Tyr Tyr Val Asn Gly Lys Pro Arg Leu Thr Ala Ile  
 340 345 350  
 Gln Thr Asp Gln Ile Gly Ser Ile Leu Trp Ala Met Asp Val His Tyr  
 355 360 365  
 Arg Leu Thr Gly Asp Arg Lys Phe Val Glu Arg Tyr Trp Asn Thr Ile  
 370 375 380  
 Glu Lys Ala Ala Asn Tyr Leu Arg Leu Val Ala Leu Asn Phe Thr Pro  
 385 390 395 400  
 Cys Phe Asp Leu Trp Glu Glu Arg Phe Gly Val Phe Ala Tyr Thr Met

405            410            415  
 Gly Ala Thr Tyr Ala Gly Leu Lys Cys Ala Tyr Ser Met Ser Lys Ala  
 420            425            430  
 Val Asn Lys Arg Asp Lys Val Lys Asp Trp Gly Lys Thr Ile Glu Phe  
 435            440            445  
 Leu Lys His Glu Val Pro Lys Arg Phe Tyr Leu Glu Asp Glu Glu Arg  
 450            455            460  
 Phe Ala Lys Ser Ile Asn Pro Leu Asp Lys Thr Ile Asp Thr Ser Ile  
 465            470            475            480  
 Leu Gly Leu Ser Tyr Pro Phe Asn Leu Ile Asp Val Asp Asp Glu Arg  
 485            490            495  
 Met Ile Lys Thr Ala Glu Ala Ile Glu Lys Ala Phe Lys Tyr Lys Val  
 500            505            510  
 Gly Gly Ile Gly Arg Tyr Pro Glu Asp Ile Tyr Phe Gly Gly Asn Pro  
 515            520            525  
 Trp Ile Ile Thr Thr Leu Trp Leu Ser Leu Tyr Tyr Arg Arg Leu Tyr  
 530            535            540  
 Lys Val Leu Lys Glu Lys Asp Asp Asn Gly Ala Asp Ile Tyr Leu Gln  
 545            550            555            560  
 Lys Ser Lys Lys Leu Phe Asn Trp Val Met Lys Tyr Ser Phe Asp Gly  
 565            570            575  
 Leu Phe Pro Glu Gln Ile His Lys Glu Leu Gly Val Pro Met Ser Ala  
 580            585            590  
 Met Pro Leu Gly Trp Ser Asn Ala Met Phe Leu Ile Tyr Val Tyr Glu  
 595            600            605  
 Asn Asp Lys Val Ile Ile Pro  
 610            615

&lt;210&gt; 11

&lt;211&gt; 2034

&lt;212&gt; DNA

&lt;213&gt; Archaea

&lt;400&gt; 11

gtggttagca tggtaggaat tattgggaat gggaaaatcc tcgcaaagat tgaatgactca 60  
 ggctctttgg aatacatatt tttccacat ttggggcatg agaacatat ttttgattca 120  
 tcatttgcca tattttatga taataagttg aaatggaatt gggacaattc ctgggatatt 180  
 aatcagaact atttaaaaga tacaacata ttgaaaacat catatgaaaa cgaggatttt 240  
 ctaatagaat caaaggacta cgtgcctata tcccataact cgataattaa gcaaatatca 300  
 atattaaaca aatccagcga aaaaaagaat taaaactgt tttttatga aaatttaaga 360  
 atgggagaaa ttctgaagt aagtactgta aagtatagaa agaacaggga gtgcattatt 420  
 aaatacgata agaattatgt ttttgtatc ggcagtaata aaaaagtatc tcataccaa 480  
 tgtggtgta ggtcatccga gagtagtgcc cttaatgatc tcaaaaatgg tattttaag 540  
 gaatacgata gtgtgaagg cctaatacaca gatagcgcac tgggttgga ccttgagttg 600  
 agtccaaatc aggaacagaa agtctcaata tttatattg cagataagta tgggtgggat 660  
 tataacaaaa ttatgaattt attggataca ctaaatatag ttataaccaa tcacgcagac 720  
 atatatgatc ttacaatggc atactggaag aacatgattg aaaccactgc gaatagtcta 780  
 tgcaattcaa atcaagtctt taaagattta acacataata aagacgacgc aaatatitca 840  
 aatttaaaaa gaataaaaca gtatgaagct atttgtaaaa gatccctatt aaccatttta 900  
 ctctttgtg atcataatgg tgaataatt gcatccat cactctatcc agattataga 960  
 tatgtatggt gtagggacgc aggttatatg gccgtgcac ttgacctatg tggtcagcat 1020

ggaataagcg aaaaatactt tgaatggtgc aaaaaaacac aaaatagtga tggctcatgg 1080  
 gttcaaaact actacgtaga aggaaatcca aggcttacgg caattcaaat tgaccaagtt 1140  
 ggtactacaa tctgggccgc acttgtacat tatagaataa ctagggacaa attattctg 1200  
 aacagatatt gggaaatgat taaaaagca ggggattatt taagtagtgt tgccaatcca 1260  
 ccatcaccaa gctatgattt atgggaagaa aaatatggtg tattcgata cacactggc 1320  
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 cacgatatcc aaaattggaa agagagcatg gacttcctta aaaacgaaat ggtagatagg 1440  
 ctttatttaa aagatgaaaa tagatttga aaatcattgg atccattga caaagctcta 1500  
 gatgctagta ttttagggct cagttttcca tataatttgg tacctgtga tgaccctaga 1560  
 atgattagca ccgccaacca aattgaaaat gcgtttaagt ataaggttgg aggtatagga 1620  
 aggtaccctg aagatgttta ttctggaggg aatccttga taataaccac aatatggctc 1680  
 catatgtact atgaaaactt gattaaatca ttatctaaac atggtaaaaa tgccatacat 1740  
 tctgatcaaa tccctgattc tcaggggac ctttaaggatt ttgtctaat tatagggtcc 1800  
 attgaaaacc atggtgaaaa gtcagatgaa acccctagt cgcacacact cttacttat 1860  
 gcccaaaaat gtaacaattt gtttgattgg actttaaagt ataacttta tgaactattt 1920  
 ccagaacagg ttcaacaaga tcttgagct cggatatctg caattccact tgggtggtca 1980  
 catgcaatgg tcataatgc catccatggt aactttgata tattaatacc ttaa 2034

&lt;210&gt; 12

&lt;211&gt; 677

&lt;212&gt; PRT

&lt;213&gt; Archaea

&lt;400&gt; 12

Met Val Ser Met Val Gly Ile Ile Gly Asn Gly Lys Ile Leu Ala Lys  
 1 5 10 15  
 Ile Asp Asp Ser Gly Ser Leu Glu Tyr Ile Phe Phe Pro His Leu Gly  
 20 25 30  
 His Glu Lys His Ile Phe Asp Ser Ser Phe Ala Ile Phe Tyr Asp Asn  
 35 40 45  
 Lys Leu Lys Trp Asn Trp Asp Asn Ser Trp Asp Ile Asn Gln Asn Tyr  
 50 55 60  
 Leu Lys Asp Thr Asn Ile Leu Lys Thr Ser Tyr Glu Asn Glu Asp Phe  
 65 70 75 80  
 Leu Ile Glu Ser Lys Asp Tyr Val Pro Ile Ser His Asn Ser Ile Ile  
 85 90 95  
 Lys Gln Ile Ser Ile Leu Asn Lys Ser Ser Glu Lys Lys Asn Leu Lys  
 100 105 110  
 Leu Phe Phe Tyr Glu Asn Leu Arg Met Gly Glu Ile Pro Glu Val Ser  
 115 120 125  
 Thr Val Lys Tyr Arg Lys Asn Arg Glu Cys Ile Ile Lys Tyr Asp Lys  
 130 135 140  
 Asn Tyr Val Phe Cys Ile Gly Ser Asn Lys Lys Val Ser Ser Tyr Gln  
 145 150 155 160  
 Cys Gly Val Arg Ser Ser Glu Ser Ser Ala Leu Asn Asp Leu Lys Asn  
 165 170 175  
 Gly Ile Leu Lys Glu Tyr Asp Ser Ala Glu Gly Leu Ile Thr Asp Ser  
 180 185 190  
 Ala Leu Gly Trp Asp Leu Glu Leu Ser Pro Asn Gln Glu Gln Lys Val  
 195 200 205  
 Ser Ile Phe Ile Phe Ala Asp Lys Tyr Gly Gly Asp Tyr Thr Lys Ile

210            215            220  
 Met Asn Leu Leu Asp Thr Leu Asn Ile Val Ile Thr Asn His Ala Asp  
 225            230            235            240  
 Ile Tyr Asp Leu Thr Met Ala Tyr Trp Lys Asn Met Ile Glu Thr Thr  
           245            250            255  
 Ala Asn Ser Leu Cys Asn Ser Asn Gln Val Phe Lys Asp Leu Thr His  
           260            265            270  
 Ile Lys Asp Asp Ala Asn Ile Ser Asn Leu Lys Arg Ile Lys Gln Tyr  
           275            280            285  
 Glu Ala Ile Cys Lys Arg Ser Leu Leu Thr Ile Leu Leu Leu Cys Asp  
           290            295            300  
 His Asn Gly Gly Ile Ile Ala Ser Pro Ser Leu Tyr Pro Asp Tyr Arg  
 305            310            315            320  
 Tyr Val Trp Cys Arg Asp Ala Gly Tyr Met Ala Val Ala Leu Asp Leu  
           325            330            335  
 Cys Gly Gln His Gly Ile Ser Glu Lys Tyr Phe Glu Trp Cys Lys Lys  
           340            345            350  
 Thr Gln Asn Ser Asp Gly Ser Trp Val Gln Asn Tyr Tyr Val Glu Gly  
           355            360            365  
 Asn Pro Arg Leu Thr Ala Ile Gln Ile Asp Gln Val Gly Thr Thr Ile  
           370            375            380  
 Trp Ala Ala Leu Val His Tyr Arg Ile Thr Arg Asp Lys Leu Phe Leu  
 385            390            395            400  
 Asn Arg Tyr Trp Glu Met Ile Lys Lys Ala Gly Asp Tyr Leu Ser Ser  
           405            410            415  
 Val Ala Asn Pro Pro Ser Pro Ser Tyr Asp Leu Trp Glu Glu Lys Tyr  
           420            425            430  
 Gly Val Phe Ala Tyr Thr Leu Gly Ala Ile Tyr Gly Gly Leu Lys Ser  
           435            440            445  
 Ala Tyr Asn Ile Cys Lys Ile Leu Gly Lys Glu Glu His Asp Ile Gln  
           450            455            460  
 Asn Trp Lys Glu Ser Met Asp Phe Leu Lys Asn Glu Met Val Asp Arg  
 465            470            475            480  
 Leu Tyr Leu Lys Asp Glu Asn Arg Phe Ala Lys Ser Leu Asp Pro Leu  
           485            490            495  
 Asp Lys Ala Leu Asp Ala Ser Ile Leu Gly Leu Ser Phe Pro Tyr Asn  
           500            505            510  
 Leu Val Pro Val Asp Asp Pro Arg Met Ile Ser Thr Ala Asn Gln Ile  
           515            520            525  
 Glu Asn Ala Phe Lys Tyr Lys Val Gly Gly Ile Gly Arg Tyr Pro Glu  
           530            535            540  
 Asp Val Tyr Phe Gly Gly Asn Pro Trp Ile Ile Thr Thr Ile Trp Leu  
 545            550            555            560  
 His Met Tyr Tyr Glu Asn Leu Ile Lys Ser Leu Ser Lys His Gly Lys  
           565            570            575  
 Asn Ala Ile His Ser Asp Gln Ile Pro Asp Ser Ser Gly Asp Leu Lys  
           580            585            590  
 Asp Phe Val Ser Ile Ile Gly Ser Ile Glu Asn His Gly Glu Lys Ser  
           595            600            605  
 Asp Glu Thr Pro Ser Ser Asp Thr Leu Leu Thr Tyr Ala Gln Lys Cys  
           610            615            620

Asn Asn Leu Phe Asp Trp Thr Leu Lys Tyr Asn Phe Asn Glu Leu Phe  
 625                      630                      635                      640  
 Pro Glu Gln Val His Lys Asp Leu Gly Ala Pro Ile Ser Ala Ile Pro  
                     645                      650                      655  
 Leu Gly Trp Ser His Ala Met Val Ile Ile Ala Ile His Gly Asn Phe  
                     660                      665                      670  
 Asp Ile Leu Ile Pro  
                     675

&lt;210&gt; 13

&lt;211&gt; 1779

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 13

atgattgttg gtaataatag cttttatgt aagatagggg atcatggaga aattgaatat 60  
 gcattctacc cccatgttgg ttatgaacta catTTTTTg atagttcttt agctatatat 120  
 gataaagaaa ttatgtggat atgggataaa gagtggagtg tatacagaa atatattgag 180  
 gacactaata tattcaaaac tactttagaa aatgagaata tcatatttgt tataaaagat 240  
 ttatgcccaa ttacacataa tgtattaatt aggagagttt tcattaaaaa taaactcca 300  
 tataattata attttaaact atttttctat gaaaatctta gaattggaga acatccttca 360  
 gaaaatacag ttaagttttt agatgattgt atagttaaatt ttaatggcaa atatactttt 420  
 tgtataagca gtgataaaaa aataaattca taccagtgtg gaaatagata tagtgaaaaa 480  
 tctgcttata aagatatga aatgggttta ttatctgaaa atcctgaaag tgttggagt 540  
 ctaactgaca gtgctattga atgggatata gatttaaaac cacatggaaa agtagcattt 600  
 aacatctaca tcttctctca tattggaaat aatatagaga ttataaaaaa tcagttaaatt 660  
 attattaaaa atctctcttc tgaaataaaa aatatatctc taaattattg gaagagttct 720  
 ttgatataa aaggttatct atttaatgaa aatatattaa aattagcaaa aagggtctta 780  
 atgatactaa caatgcttcc tgacaaaaat ggaggaatta tagcctctcc atctattcat 840  
 cctgattata gatattgttg gggtagagat ggaagtata tggctgtggc attatccatt 900  
 tatggaataa aaaacattcc atggagggtc ttccatttca tgctaaagt ccagaatctt 960  
 gatggttcat gggtacaaaa ctattataca gatggtaaac caagattaac tgccttaca 1020  
 atagatcaaa taggttcagt tctttgggct atggaagttt attatagaac tacagggtgat 1080  
 agagagtttg ttaaaaaatt ctgggaaact attgagaaag ctggaaattt cttatataat 1140  
 gcttcattat ctttaatgcc atgttttgat ctttgggaag aaaaatatgg ggtattttca 1200  
 tatactttag gagcaatgta tggaggatta agggcaggat gtagttagc taaagctata 1260  
 gaagagaaaa aagaagattg gaaaaaggct ttatataaat taaagaagga tgttgattta 1320  
 ttatatataa gtgatgaaga aagatttgtt aaatctatta acccattgaa caaagagatt 1380  
 gatacaagta tattagggct tagctatcca ttggactag ttaaagttaa tgatgaaaga 1440  
 atgataaaaa ctgctgaagc catagaaaaa gcttttaaat acaaagttgg aggtattggg 1500  
 agatatccat ctgatgttta ttttgaggga aatccttga ttataacaac actttgggtta 1560  
 gctttatatt atagaagact atttattact acaaatgata gaaaatattt agaaaaatca 1620  
 aaaaagctat ttaattgggt tattaacct atctatctat tcctgaaca gatacataaa 1680  
 gaattagcta ttctgtatc agctatgct ttagggtgga gttgtgctat gctgttattc 1740  
 tatctatata aaaatgatga cataatagt ataaaatga 1779

&lt;210&gt; 14

&lt;211&gt; 592



&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 14

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Met Ile Val Gly Asn Asn Ser Phe Leu Cys Lys Ile Gly Asp His Gly
      5           10           15
Ile Glu Tyr Ala Phe Tyr Pro His Val Gly Tyr Glu Leu His Phe
      20           25           30
Phe Asp Ser Ser Leu Ala Ile Tyr Asp Lys Glu Ile Met Trp Ile Trp
      35           40           45
Lys Glu Trp Ser Val Tyr Gln Lys Tyr Ile Glu Asp Thr Asn Ile
      55           60
Lys Thr Thr Leu Glu Asn Glu Asn Ile Ile Phe Val Ile Lys Asp
      70           75           80
Leu Val Pro Ile Ser His Asn Val Leu Ile Arg Arg Val Phe Ile Lys
      85           90           95
Asn Lys Leu Pro Tyr Asn Tyr Asn Phe Lys Leu Phe Phe Tyr Glu Asn
      100          105          110
Leu Arg Ile Gly Glu His Pro Ser Glu Asn Thr Val Lys Phe Leu Asp
      115          120          125
Asp Cys Ile Val Lys Phe Asn Gly Lys Tyr Thr Phe Cys Ile Ser Ser
      130          135          140
Asp Lys Lys Ile Asn Ser Tyr Gln Cys Gly Asn Arg Tyr Ser Glu Lys
      145          150          155          160
Ser Ala Tyr Lys Asp Ile Glu Asn Gly Leu Leu Ser Glu Asn Pro Glu
      165          170          175
Ser Val Gly Val Leu Thr Asp Ser Ala Ile Glu Trp Asp Ile Asp Leu
      180          185          190
Lys Pro His Gly Lys Val Ala Phe Asn Ile Tyr Ile Phe Pro His Ile
      195          200          205
Gly Asn Asn Ile Glu Ile Ile Lys Asn Gln Leu Asn Ile Ile Lys Asn
      210          215          220
Leu Ser Ser Glu Ile Lys Asn Ile Ser Leu Asn Tyr Trp Lys Ser Ser
      225          230          235          240
Phe Asp Ile Lys Gly Tyr Leu Phe Asn Glu Lys Tyr Leu Lys Leu Ala
      245          250          255
Lys Arg Ala Leu Met Ile Leu Thr Met Leu Ser Asp Lys Asn Gly Gly
      260          265          270
Ile Ile Ala Ser Pro Ser Ile His Pro Asp Tyr Arg Tyr Val Trp Gly
      275          280          285
Arg Asp Gly Ser Tyr Met Ala Val Ala Leu Ser Ile Tyr Gly Ile Lys
      290          295          300
Asn Ile Pro Trp Arg Phe Phe His Phe Met Ser Lys Val Gln Asn Leu
      305          310          315          320
Asp Gly Ser Trp Leu Gln Asn Tyr Tyr Thr Asp Gly Lys Pro Arg Leu
      325          330          335
Thr Ala Leu Gln Ile Asp Gln Ile Gly Ser Val Leu Trp Ala Met Glu
      340          345          350

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Val Tyr Tyr Arg Thr Thr Gly Asp Arg Glu Phe Val Lys Lys Phe Trp  
 355 360 365  
 Glu Thr Ile Glu Lys Ala Gly Asn Phe Leu Tyr Asn Ala Ser Leu Ser  
 370 375 380  
 Leu Met Pro Cys Phe Asp Leu Trp Glu Glu Lys Tyr Gly Val Phe Ser  
 385 390 395 400  
 Tyr Thr Leu Gly Ala Met Tyr Gly Gly Leu Arg Ala Gly Cys Ser Leu  
 405 410 415  
 Ala Lys Ala Ile Glu Glu Lys Lys Glu Asp Trp Lys Lys Ala Leu Asp  
 420 425 430  
 Lys Leu Lys Lys Asp Val Asp Leu Leu Tyr Leu Ser Asp Glu Glu Arg  
 435 440 445  
 Phe Val Lys Ser Ile Asn Pro Leu Asn Lys Glu Ile Asp Thr Ser Ile  
 450 455 460  
 Leu Gly Leu Ser Tyr Pro Phe Gly Leu Val Lys Val Asn Asp Glu Arg  
 465 470 475 480  
 Met Ile Lys Thr Ala Glu Ala Ile Glu Lys Ala Phe Lys Tyr Lys Val  
 485 490 495  
 Gly Gly Ile Gly Arg Tyr Pro Ser Asp Val Tyr Phe Gly Gly Asn Pro  
 500 505 510  
 Trp Ile Ile Thr Thr Leu Trp Leu Ala Leu Tyr Tyr Arg Arg Leu Phe  
 515 520 525  
 Ile Thr Thr Asn Asp Arg Lys Tyr Leu Glu Lys Ser Lys Lys Leu Phe  
 530 535 540  
 Asn Trp Val Ile Asn His Ile Tyr Leu Phe Pro Glu Gln Ile His Lys  
 545 550 555 560  
 Glu Leu Ala Ile Pro Val Ser Ala Met Pro Leu Gly Trp Ser Cys Ala  
 565 570 575  
 Met Leu Leu Phe Tyr Leu Tyr Lys Asn Asp Asp Ile Ile Val Ile Lys  
 580 585 590

&lt;210&gt; 15

&lt;211&gt; 2121

&lt;212&gt; DNA

&lt;213&gt; Bacterial

&lt;400&gt; 15

atgaaattga atagaaaact tataaaatat ttaccctgtac tatttcttgc gtccagtgtg 60  
 ctaagtggat gcgctaacaa taatatatca aacattaaaa ttgagagatt gaataatgta 120  
 caagcagtaa atggccctgg agaggctgat acttgggcta aagctcagaa acaaggtgta 180  
 gggactgcaa acaactatac ttcaaagta tggttacca ttgcagacgg ggggatatct 240  
 gaggttact atccgactat agatactgct gatgtaaagg atattaaatt tttgtgaca 300  
 gatggaaaaa cgtttgtctc agatgagaca aaagacacaa taaccaaaagt cgaaaagttt 360  
 actgaaaaat cgttgggcta taaaatcatt aacacagata aagaaggagg atataagata 420  
 actaaagaaa tatttacgga tgtaaaggagg aattctctcg taattaaaac gaagtttgaa 480  
 gccttaaaag gcaatgttga tgattacagg ctttacgtaa tgtgtgatcc tcatgtaaaa 540  
 aatcagggca aatataatga aggatatgca gtaaggcaa atggcaatgt tgcgctaatt 600  
 gctgaaagag atggaattta cactgcattg tcatctgaca taggatggaa aaagtattcg 660  
 atagggtatt ataaagtaaa tgacattgag accgatcttt ataaaaatat gcaaatgact 720  
 tacaattacg acagtgaag aggcaacatc atagaagggtg ctgagataga tcttaagaaa 780  
 aacaggcaat ttgaaatcgt tctgtcttcc ggacagagtg aagacgaggc agtaaaaaaca 840

aacatggaaa ctttaaatga taattatgac agcttaaaga aagcgtatat agaccaatgg 900  
 gagaagtatt gcgatagcct taatgacttt ggaggaaaag caaattcact gtattttaac 960  
 agtatgatga tattaaaggc cagtgaagac aagacaaaaca aagggtgcta tatagcatcg 1020  
 ctatctattc cgtgggggtga tggccaagaa gatgacaata ttggtggcta ccatctcgta 1080  
 tggtaagag atctgtacca ttagcgaat gcattattg ttgctggga tactgattcg 1140  
 gcaaatagag cactggatta ttagacaaa gtagtgaaag acaatggaat gattcctcaa 1200  
 aatacatgga taaatggag gccttattgg acaggcatac agcttgatga gcaggcggat 1260  
 ccaataatat taagtatat gttgaaaaga tacgattctt atgaaagtct tgttaagcct 1320  
 ttggcggatt tcatcatgaa aataggccct aagacgggac aagaaagatg ggaagaaata 1380  
 ggtggatatt cgccagcaac attggcttca gaagtagctg gacttacatg tgctgcgtat 1440  
 atagctgaac aaaataagga ctttgaatct gctaaaaaat atcaagaaaa ggccggataat 1500  
 tggcaaaggc ttattgacaa cctaacttac acagaaaaag gccattggg agatggtcac 1560  
 tattatataa gtagatcagg gctccagat ccaaatgccg atttcatgat aagcatagcg 1620  
 aatggcgggtg gtgtatacga ccaaaaagaa atcgtggatc caagttttct ggaacttgta 1680  
 aggcttggag taaatcagc agatgacctt aaaatactaa atacgtgaa agtcgtggat 1740  
 gaaacaataa aagtcgatac accgaaagga ccatcatggt ataggtataa tcatgatgga 1800  
 tatggtgaga tgttaagac agaactatat catgggacag gaaaaggaag attgtggcca 1860  
 ctgcttacag gtgagagagg catgtacgaa attgtgcag agtatgatga tgtaataatt 1920  
 ataaagacaa gaatagggtt attgaaaggc tcaaggataa gatttgagta cgatatagtg 1980  
 aaagaagatg aaaataagct ttagcaciaa ggtatgacag aacacccatt tacgacactt 2040  
 gacagaaaac ctgtaatat aaaaaagatt tgcctcatg ttatgaaat gttgaacaaa 2100  
 tgctatgatg atggtgttta g 2121

&lt;210&gt; 16

&lt;211&gt; 706

&lt;212&gt; PRT

&lt;213&gt; Bacterial

&lt;400&gt; 16

Met Lys Leu Asn Arg Lys Leu Ile Lys Tyr Leu Pro Val Leu Phe Leu  
 1 5 10 15  
 Ala Ser Ser Val Leu Ser Gly Cys Ala Asn Asn Asn Ile Ser Asn Ile  
 20 25 30  
 Lys Ile Glu Arg Leu Asn Asn Val Gln Ala Val Asn Gly Pro Gly Glu  
 35 40 45  
 Ala Asp Thr Trp Ala Lys Ala Gln Lys Gln Gly Val Gly Thr Ala Asn  
 50 55 60  
 Asn Tyr Thr Ser Lys Val Trp Phe Thr Ile Ala Asp Gly Gly Ile Ser  
 65 70 75 80  
 Glu Val Tyr Tyr Pro Thr Ile Asp Thr Ala Asp Val Lys Asp Ile Lys  
 85 90 95  
 Phe Phe Val Thr Asp Gly Lys Thr Phe Val Ser Asp Glu Thr Lys Asp  
 100 105 110  
 Thr Ile Thr Lys Val Glu Lys Phe Thr Glu Lys Ser Leu Gly Tyr Lys  
 115 120 125  
 Ile Ile Asn Thr Asp Lys Glu Gly Arg Tyr Lys Ile Thr Lys Glu Ile  
 130 135 140  
 Phe Thr Asp Val Lys Arg Asn Ser Leu Val Ile Lys Thr Lys Phe Glu  
 145 150 155 160  
 Ala Leu Lys Gly Asn Val Asp Asp Tyr Arg Leu Tyr Val Met Cys Asp  
 165 170 175

Pro His Val Lys Asn Gln Gly Lys Tyr Asn Glu Gly Tyr Ala Val Lys  
 180 185 190  
 Ala Asn Gly Asn Val Ala Leu Ile Ala Glu Arg Asp Gly Ile Tyr Thr  
 195 200 205  
 Ala Leu Ser Ser Asp Ile Gly Trp Lys Lys Tyr Ser Ile Gly Tyr Tyr  
 210 215 220  
 Lys Val Asn Asp Ile Glu Thr Asp Leu Tyr Lys Asn Met Gln Met Thr  
 225 230 235 240  
 Tyr Asn Tyr Asp Ser Ala Arg Gly Asn Ile Ile Glu Gly Ala Glu Ile  
 245 250 255  
 Asp Leu Lys Lys Asn Arg Gln Phe Glu Ile Val Leu Ser Phe Gly Gln  
 260 265 270  
 Ser Glu Asp Glu Ala Val Lys Thr Asn Met Glu Thr Leu Asn Asp Asn  
 275 280 285  
 Tyr Asp Ser Leu Lys Lys Ala Tyr Ile Asp Gln Trp Glu Lys Tyr Cys  
 290 295 300  
 Asp Ser Leu Asn Asp Phe Gly Gly Lys Ala Asn Ser Leu Tyr Phe Asn  
 305 310 315 320  
 Ser Met Met Ile Leu Lys Ala Ser Glu Asp Lys Thr Asn Lys Gly Ala  
 325 330 335  
 Tyr Ile Ala Ser Leu Ser Ile Pro Trp Gly Asp Gly Gln Glu Asp Asp  
 340 345 350  
 Asn Ile Gly Gly Tyr His Leu Val Trp Ser Arg Asp Leu Tyr His Val  
 355 360 365  
 Ala Asn Ala Phe Ile Val Ala Gly Asp Thr Asp Ser Ala Asn Arg Ala  
 370 375 380  
 Leu Asp Tyr Leu Asp Lys Val Val Lys Asp Asn Gly Met Ile Pro Gln  
 385 390 395 400  
 Asn Thr Trp Ile Asn Gly Arg Pro Tyr Trp Thr Gly Ile Gln Leu Asp  
 405 410 415  
 Glu Gln Ala Asp Pro Ile Ile Leu Ser Tyr Arg Leu Lys Arg Tyr Asp  
 420 425 430  
 Leu Tyr Glu Ser Leu Val Lys Pro Leu Ala Asp Phe Ile Met Lys Ile  
 435 440 445  
 Gly Pro Lys Thr Gly Gln Glu Arg Trp Glu Glu Ile Gly Gly Tyr Ser  
 450 455 460  
 Pro Ala Thr Leu Ala Ser Glu Val Ala Gly Leu Thr Cys Ala Ala Tyr  
 465 470 475 480  
 Ile Ala Glu Gln Asn Lys Asp Phe Glu Ser Ala Lys Lys Tyr Gln Glu  
 485 490 495  
 Lys Ala Asp Asn Trp Gln Arg Leu Ile Asp Asn Leu Thr Tyr Thr Glu  
 500 505 510  
 Lys Gly Pro Leu Gly Asp Gly His Tyr Tyr Ile Arg Ile Ala Gly Leu  
 515 520 525  
 Pro Asp Pro Asn Ala Asp Phe Met Ile Ser Ile Ala Asn Gly Gly Gly  
 530 535 540  
 Val Tyr Asp Gln Lys Glu Ile Val Asp Pro Ser Phe Leu Glu Leu Val  
 545 550 555 560  
 Arg Leu Gly Val Lys Ser Ala Asp Asp Pro Lys Ile Leu Asn Thr Leu  
 565 570 575  
 Lys Val Val Asp Glu Thr Ile Lys Val Asp Thr Pro Lys Gly Pro Ser

580 585 590  
Trp Tyr Arg Tyr Asn His Asp Gly Tyr Gly Glu Met Ser Lys Thr Glu  
595 600 605  
Leu Tyr His Gly Thr Gly Lys Gly Arg Leu Trp Pro Leu Leu Thr Gly  
610 615 620  
Glu Arg Gly Met Tyr Glu Ile Ala Ala Glu Tyr Asp Asp Val Ile Ile  
625 630 635 640  
Ile Lys Thr Arg Ile Gly Leu Leu Lys Gly Ser Arg Ile Arg Phe Glu  
645 650 655  
Tyr Asp Ile Val Lys Glu Asp Glu Asn Lys Leu Leu Ala Gln Gly Met  
660 665 670  
Thr Glu His Pro Phe Thr Thr Leu Asp Arg Lys Pro Val Asn Ile Lys  
675 680 685  
Lys Ile Leu Pro His Val Tyr Glu Met Leu Asn Lys Cys Tyr Asp Asp  
690 695 700  
Gly Val  
705

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